#7B

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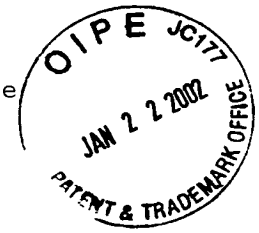

<110> de la Monte, Suzanne

Wands, Jack R.

<120> Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease

<130> 0609.4370002

<140> 09/964,678

<141> 2001-09-28

<150> 09/380,203

<151> 2000-04-25

<150> PCT/US98/03685

<151> 1998-02-26

<150> 60/038,908

<151> 1997-02-26

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<170> PatentIn version 3.1

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Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
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gat tct cct gcc tca gcc tcc cca gta gct ggg att aca ggc atg tgc       146
Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
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acc cac gct cgg cta att ttg tat ttt ttt tta gta gag atg gag ttt       194
Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
45                  50                  55                  60

ctc cat gtt ggt cag gct ggt ctc gaa ctc ccg acc tca gat gat ccc       242
Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
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tcc gtc tcg gcc tcc caa agt gct aga tac agg act ggc cac cat gcc       290
Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala
            80                  85                  90

cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gtt tca ctg atg       338
Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met
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tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ctc agc ctc       386
Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu
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cca aag tgc tgg gat tac agg cgt gca gcc gtg cct ggc ctt ttt att       434
Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile
125                 130                 135                 140

tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg       482
Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val
                145                 150                 155

cag tgg tgt gat cac agc tca ctg cag cct tca act cct gag atc aag       530
Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys
            160                 165                 170

cat cct cct gcc tca gcc tcc caa gta gct ggg acc aaa gac atg cac       578
His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His
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His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln
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agt ctc aac tct gtc acc cag gct gga gtg cag tgg cgc aat ctt ggc      674
Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly
205                 210                 215                 220

tca ctg caa cct ctg cct ccc ggg ttc aag tta ttc tcc tgc ccc agc      722
Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser
                225                 230                 235

ctc ctg agt agc tgg gac tac agg cgc cca cca cgc cta gct aat ttt      770
Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe
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Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile
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ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct      866
Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala
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ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt      914
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
285                 290                 295                 300

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Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
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cca aat ctc ggc tca ctg caa cct ctg cct ccc ggg ctc aag cga ttc     1010
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
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Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
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cac ccc gct aat ttt tgt att ttc att aga ggc ggg gtt tca cca tat     1106
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
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Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
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35 40 45

Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
50 55 60

Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
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Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
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Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
100 105 110

Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
115 120 125

Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
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Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
145 150 155 160

His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
165 170 175

Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
180 185 190

Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
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